


```

OY 181 RTQEAIVWVYSDNAPISNPDESFRSESNVSTSOISLMROAKOLIDPNATKMPKOV 240
DB 181 RTQEAIVWVYSDNAPISNPDESFRSESNVSTSOISLMROAKOLIDPNATKMPKOV 240
OY 241 PDFOLSTFESBDEKGRKYNKYONLSSGLVPTKPTPGDPMPAPQPTOTSLIKKYAI 300
DB 241 PDFOLSTFESBDEKGRKYNKYONLSSGLVPTKPTPGDPMPAPQPTOTSLIKKYAI 300
OY 301 GDYSKLEGGATLOLTGDVNNSFOARVSSNDIGERIELSDGYTTLTSLNTPAGYSTAEP 360
DB 301 GDYSKLEGGATLOLTGDVNNSFOARVSSNDIGERIELSDGYTTLTSLNTPAGYSTAEP 360
OY 361 TFEVVEAGKYTTIIDGQOENPNKEIPEYSVEAYNDEEFVYLTONTAKFYAKKNKS 420
DB 361 TFEVVEAGKYTTIIDGQOENPNKEIPEYSVEAYNDEEFVYLTONTAKFYAKKNKS 420
OY 421 SOVVYCFNADLKSPPESEDEGKTMPTDFTGEKYYHIGRDLFEKTYVPRDTPDTFLK 480
DB 421 SOVVYCFNADLKSPPESEDEGKTMPTDFTGEKYYHIGRDLFEKTYVPRDTPDTFLK 480
OY 481 HIKKVIKGYREKQAIEXSGLTETOLRAATOLAIYFTDSAEIDKDKLDYHGFQDMND 540
DB 481 HIKKVIKGYREKQAIEXSGLTETOLRAATOLAIYFTDSAEIDKDKLDYHGFQDMND 540
OY 541 STLAAKILVEYAODSNPQOLTDLPFFINNNKYGSLIGTQWHPEDVDIIMEDKKEVI 600
DB 541 STLAAKILVEYAODSNPQOLTDLPFFINNNKYGSLIGTQWHPEDVDIIMEDKKEVI 600
OY 601 PTHNLTLRKTYTGLAGDRTKDFHFEIELKNNKOELLSTQVTKDKNLEFKGKATINLK 660
DB 601 PTHNLTLRKTYTGLAGDRTKDFHFEIELKNNKOELLSTQVTKDKNLEFKGKATINLK 660
OY 661 HGSILTLQGLPEGYSTLVKETDESEGYKVNQSOEVANATVSKTIGTSDETLAFENNKKEV 720
DB 661 HGSILTLQGLPEGYSTLVKETDESEGYKVNQSOEVANATVSKTIGTSDETLAFENNKKEV 720
OY 721 VPTGVOKINGYALIVAGISLIGTIGTIGTIRIKRHD 757
DB 721 VPTGVOKINGYALIVAGISLIGTIGTIGTIRIKRHD 757

RESULT 2
O8RP53 PRELIMINARY: PRT: 756 AA.
AC 08RP53;
DT 01-JUN-2002 (TREMELREL. 21, Created)
DT 01-JUN-2002 (TREMELREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMELREL. 21, Last annotation update)
DE Cpa.
GN CPA.12.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A735;
RX MEDLINE-21843101; PubMed-11854196;
RA Bessen D.E., Kalla A.;
RT "Genomic localization of a T serotype locus to a recombinatorial zone
RT encoding extracellular matrix-binding proteins in Streptococcus
RT pyogenes."
RL Infect. Immun. 70:1159-1167(2002).
DR EMBL: AF447492; FAL86406.1; -.
SQ SEQUENCE 756 AA; 85698 MW; 88BDE087714EC464 CRC64;

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Query Match 52.2%; Score 2058.5; DB 2: Length 756;
 Best Local Similarity 54.3%; Pred. No. 1.2e-105;
 Matches 404; Conservative 126; Mismatches 189; Indels 25; Gaps 10;

OY 17 RVLSNKRFTVTLVGVFLMFLATVTSNMGAKTVG---LVESSTPNAINPDSSEYRW 72
 DB 14 RVSNRKPQLVTLVGVFLMFLATVTSNMGAKTVG---LVESSTPNAINPDSSEYRW 72

Med Aug 20 11:56:16

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OY 73 YGESYVRGHPYKQFRAVHDLRVNLGESSRYOVYCFNLKKAFLPLGSDSVYKWKYKHDG 132
DB 72 YGDSYDSHPPYKQFRAVHDLRVNLGESSRYOVYCFNLKKAFLPLGSDSVYKWKYKHDG 131
OY 133 ISTKEDYAMSFRITGDELNOKLRAVMTNGHPQANAMEGIEPLINAIKTVQEAIVWVYSD 192
DB 132 TGDVFTNQAQPKIGESILNNKLISIMYNAVKNKANGYMDKIEPLINAIKTVQEAIVWVYSD 191
OY 193 NAPISNPDESFRSESNVSTSOISLMROAKOLIDPNATKMPKOVDPDFOLSTFESB 252
DB 192 SS-YGNITTLWASELKDCKIDPEOVKLMREAVSKLISDLEETSKNKLPQGSKNTITVPQ 250
OY 253 DKGDYKNGYONLSSGLVPTKPTPGDPMPAPQPTOTSLIKKYAIGDYSKLEGGATL 312
DB 251 D-----KSVONLSAEVYPPESPAPQSPPEPPQTKTSYIIRKYGAGDYSKLEGGATL 304
OY 313 OLTGDVNNSFOARVSSNDIGERIELSDGYTTLTSLNTPAGYSTAEPITFEVVEAGKYTTI 372
DB 305 RLTEGDIIDFQEKVYQOSNGTEKIELSNGYVTLTETSSPDGYKIAEPIKFRVYKKNKKEVI 364
OY 373 -IDGQOENPNKEIPEYSVEAYNDEEFVYLTONTAKFYAKKNKSQOVVYCFN 428
DB 365 OKDSQVBNPNKEVAPESVVEAYSDMODSNINPEFTTPYKIFYAKKNKDSQOVVYCFN 424
OY 429 ADLKSPPESEDEGKTMPTDFTT-GEVYKTHAGDLFEKTYVPRDTPDTFLKHIKKYIE 487
DB 425 ADLHSPPESEDEGKTMPTDFTT-GEVYKTHAGDLFEKTYVPRDTPDTFLKHIKKYIE 484
OY 488 KGYRKKQAIEXSGLTETOLRAATOLAIYFTDSAEIDKDKL---KDYHGFQDMNDSTL 543
DB 485 KGYRKKQAIEXSGLTETOLRAATOLAIYFTDSAEIDKDKL---KDYHGFQDMNDSTL 542
OY 544 AVAKILVEYAODSNPQOLTDLPFFINNNKYGSLIGTQWHPEDVDIIMEDKKEVI 602
DB 543 AVTKELIYAADNSAPQOLTDLPFFINNNKYGSLIGTQWHPEDVDIIMEDKKEVI 602
OY 603 THNLTLRKTYTGLAGDRTKDFHFEIELKNNKOELLSTQVTKDKNLEFKGKATINLK 662
DB 603 THSLTVKKTYYGELGDKTKGFQFELELDKTCGPVYVTKLNNODVLAOKGKYSFNLKHG 662
OY 663 ESILTLQGLPEGYSTLVKETDESEGYKVNQSOEVANATVSKTIGTSDETLAFENNKKEV 722
DB 663 DTIRIEGLPTGYSTLVKETDEKADIVYVNNQSOEASASBNVYADKEVYFENKRDVLP 722
OY 723 TGVODKINGYALIVAGISLIGTIGTIGTIRIKRHD 746
DB 723 TGVODKINGYALIVAGISLIGTIGTIGTIRIKRHD 746

RESULT 3
O9ZB47 PRELIMINARY: PRT: 742 AA.
AC 09ZB47;
DT 01-MAY-1999 (TREMELREL. 10, Created)
DT 01-MAY-1999 (TREMELREL. 10, Last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
DE Cpa.
GN CPA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CS101;
RX Poddelski A., Moischnik M., Leonard B.A.B., Schmidt K.H.;
RA "Characterization of mta, a global negative regulator gene in group A
RT streptococci."
RL Mol. Microbiol. 31:0-0(1999).
DR EMBL: U49397; AAC97148.1; -.
SQ SEQUENCE 742 AA; 83683 MW; 97A1FF44B4BCB944 CRC64;

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